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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 13:30:07 ; Search time 30.6857 Seconds
(without alignments)
2457.601 Million cell updates/sec

Title: US-09-807-933B-3
Perfect score: 2020
Sequence: 1 MKPRTTSSMLALALGTEM.....TYKEVTCPEKITATKGSRK 366

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	782.5	38.7	219	Q9JH92	Q9JH92 unclassified
2	779.5	38.6	410	Q9P868	Q9P868 ptiromyces e
3	778.5	38.5	220	Q9JH84	Q9JH84 unclassified
4	777.5	38.5	219	Q9JH91	Q9JH91 unclassified
5	771.5	38.2	219	Q9JH87	Q9JH87 unclassified
6	769	38.1	220	Q9JH83	Q9JH83 unclassified
7	767.5	38.0	219	Q9JH89	Q9JH89 unclassified
8	764.5	37.8	217	Q9JH90	Q9JH90 unclassified
9	763.5	37.8	219	Q9JH95	Q9JH95 unclassified
10	762.5	37.7	220	Q9JH93	Q9JH93 unclassified
11	759.5	37.6	219	Q9JH88	Q9JH88 unclassified
12	756.5	37.5	219	Q9JH86	Q9JH86 unclassified
13	754.5	37.4	221	Q9JH94	Q9JH94 unclassified
14	748	37.0	218	Q9JH85	Q9JH85 unclassified
15	744.5	36.9	220	Q9JH96	Q9JH96 unclassified
16	682	33.8	305	Q93782	Q93782 humicola gr

17	625	30.9	227	3	Q93783	Q93783 humicola gr
18	576.5	28.5	271	3	Q9UV93	Q9UV93 alternaria
19	564	27.9	242	5	Q97401	Q97401 phaeodon coc
20	362.5	17.9	112	14	Q9JH80	Q9JH80 unclassified
21	361.5	17.9	112	14	Q9JH99	Q9JH99 unclassified
22	358.5	17.7	112	14	Q9JH98	Q9JH98 unclassified
23	349.5	17.3	112	14	Q9JH81	Q9JH81 unclassified
24	348.5	17.3	112	14	Q9JH82	Q9JH82 unclassified
25	335	16.6	111	14	Q9JH97	Q9JH97 unclassified
26	327	16.2	197	3	Q9P7P1	Q9P7P1 schizosacch
27	227.5	11.3	471	3	Q9HE18	Q9HE18 trichoderma
28	216.5	10.7	493	3	Q9P8D0	Q9P8D0 trichoderma
29	194	9.6	439	3	Q8WZ17	Q8WZ17 penicillium
30	193	9.6	476	3	Q92401	Q92401 agaricus bi
31	190	9.4	439	3	Q9C189	Q9C189 humicola in
32	188	9.3	439	3	Q9P893	Q9P893 agaricus bi
33	178	8.8	444	3	Q96VU2	Q96VU2 lentinula e
34	173.5	8.6	410	3	Q12665	Q12665 penicillium
35	172	8.5	443	3	Q9C1R4	Q9C1R4 lentinula e
36	171.5	8.5	290	3	Q9HE20	Q9HE20 phanerocha
37	167.5	8.3	408	3	Q9HE21	Q9HE21 phanerocha
38	167.5	8.3	408	3	Q9HE21	Q9HE21 phanerocha
39	167.5	8.3	418	3	Q93833	Q93833 trichoderma
40	167	8.3	457	3	Q93837	Q93837 acromonium
41	166.5	8.2	290	3	Q9HEY9	Q9HEY9 phanerocha
42	165.5	8.2	438	3	Q9NGR2	Q9NGR2 tetrahymena
43	160.5	7.9	536	3	Q9UVS8	Q9UVS8 aspergillus
44	160.5	7.9	1704	5	Q94446	Q94446 chironomus
45	159	7.9	823	3	Q74203	Q74203 phanerocha

ALIGNMENTS

RESULT 1

Q9JH92 PRELIMINARY; PRT; 219 AA.
ID Q9JH92
AC Q9JH92;
DT 01-OCT-2000 (TRENBLREL. 15. Created)
DT 01-OCT-2000 (TRENBLREL. 15. Last sequence update)
DT 01-MAR-2002 (TRENBLREL. 20. Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB045171; BAA98041.1; -.
DR HSSP; P43316; ZENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 219 AA; 23001 MW; 5F2EB81ADB926CE CRC64;

Query Match 38.7%; Score 782.5; DB 14; Length 219;
Best Local Similarity 67.1%; Pred. No. 1.2e-46;
Matches 139; Conservative 27; Mismatches 36; Indels 5; Gaps 3;
QY 160 NGVTRRYWDCKKACSGWPKKANNVSPVSKCKDKGVTLA-SDSNVSGGNGGNSVWCNDNQ 218
DB 16 SGRTRRYWDCKKACSGWPKKANNVSPVSKCKDKGVTLA-SDSNVSGGNGGNSVWCNDNQ 75
QY 219 PMAVNDNLAYFAAALISGSGSRWCCSFELTFTSTVAKKMWIQVNTNGDGLGSSSTG 278
DB 76 PMAVNDNLAYFAAALISGSGSRWCCSFELTFTSTVAKKMWIQVNTNGDGLGSSSTG 132
QY 279 AHFDLQMPGQGVGIFNGSKKMGAPNDGSGRYGSISSASDCSSLPALQAGCKRPFWF 338
DB 133 -QFDLAIQGGVGIVNGCTQSGAPADGMSRGVSSRSRSCSOLPSGLQAGCQWRPFWF 191

OY 339 KNAADNPSMTYKEVTCPEKITAKTGCGR 365
 DB 192 QNAADNPSINFNOYTCPEKITAKTNCGR 218

RESULT 2

O9P868 PRELIMINARY; PRT; 410 AA.

AC O9P868; PRELIMINARY; 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Endoglucanase 45A.
 GN CEL45A.
 OS Pirmomyces equi.
 OC Eukaryota; Fungi; Chytridiomycota; Neocallimastixales;
 OC Neocallimastixaceae; Pirmomyces.
 OX NCBI_TaxId=99929;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20391845; PubMed=10931904;
 RA Eberhardt R.Y., Gilbert H.J., Hazlewood G.P.;
 RT "Primary sequence and enzymatic properties of two modular
 endoglucanases, Cel5A and Cel45A, from the anaerobic fungus Pirmomyces
 equi.";
 RL Microbiology 146:1999-2008 (2000).
 DR EMBL; AJ277482; CAB92325.1; -;
 DR HSSP; P43316; 2ENG.
 DR InterPro; IPR002883; CBD 5.
 DR InterPro; IPR000334; GH 45.
 DR Pfam; PF02013; CBM_10; 3.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1
 SQ SEQUENCE 410 AA; 44380 MW; DB13BD9CFD8238DC CRC64;

Query Match 38.6%; Score 779.5; DB 3; Length 410;
 Best Local Similarity 40.7%; Pred. No. 3.6e-46;
 Matches 168; Conservative 52; Mismatches 116; Indels 77; Gaps 14;

OY 12 LALALGTEMASAKCSKLYGCGGKDMNGPTCCSGSTCKVSN----- 54
 DB 1 MRALITSCIALAASIAKVASAQAQOS--QGVNCCNPPSTVEYTDASGQGVNGQWCGI 59
 OY 55 DY-VSQCCLAPES--NGNKSSECSKLYGCGGKDMNGPTCCSGSTCKVSN DYSCCLAPES 112
 DB 60 DYSVQONQGNESCTGNSGYPCCNTC--CATYTDGQDMAFENGNNCGIKNSCKQO---PON 115
 OY 113 NGNKTSESAHKTYYY-----TAPAKEITTTAKASNSSSSG 148
 DB 116 NNQCTGNGAYRCNCQTATYTDNEGKMAFENGDMCGIKYSCPSQOVTITRTTTTQQ 175
 OY 149 KSIYVSGASS-----NGVTRYMDCKKASCSMPGKA---NVSSEPKSCNDGV 194
 DB 176 QOPPTSGGSGSNVPLNPPPSGQGTGTTTYMDCCCLASCMQNCNNDAGQVVRSCNDGI 235
 OY 195 TALSD--SN--VQSGCNGNSYMCNDNOPAVAVNDLAVGPAALISGGSESRMCCSEEL 250
 DB 236 TPTTDLNLMRYKSGGNGSVCMCDQPFMAINDVAVGFAVS-----HEKCTCORTL 288
 OY 251 TTTSTSVAKKAVIQVTTNGGLGSSSTAHPDLQMPGGVGI FNGCSKMGAPNDGMSR 310
 DB 289 KPTSGIADKQMTIVQTTNGGLGSSN--HFDIQMGGGFGIGFDGCTGQFGSGVQ--WGER 344
 OY 311 YGSISSASDCSSLPASALQAGKRWFMFQADNPSMTYKEVTCPEKITAKTGC 363
 DB 345 YGSISSASQCANLPQPKAGCEWRFMFQADNPAVAFVRVQCPRELTEITGIC 397

RESULT 3
 ID O9JH84 PRELIMINARY; PRT; 220 AA.
 AC O9JH84;

DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxId=42452;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Ohno K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus";
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB045179; BAA98049.1; -;
 DR HSSP; P43316; 2ENG.
 DR InterPro; IPR000334; GH 45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 SQ SEQUENCE 220 AA; 23274 MW; 26AF5357512EA061 CRC64;

Query Match 38.5%; Score 778.5; DB 14; Length 220;
 Best Local Similarity 64.2%; Pred. No. 2.2e-46;
 Matches 138; Conservative 31; Mismatches 41; Indels 5; Gaps 3;

OY 152 IVSGASGNGVTRRYMDCKKASGMPGKANVSPYKSCNKDGVTAL--SDSNVQSGCNGN 210
 DB 9 LISWVGDSGRTRRYMDCKKASGMPGKANVSPYKSCNKDGVTAL--SDSNVQSGCNGN 210
 OY 211 SYMCNDNQPAVAVNDNLAVGPAALISGGSESRMCCSEELTTSVAKKAVIQVTTNG 270
 DB 69 GYMVYDQAPVAVNDNLAVGPAALISGGSESRMCCSEELTTSVAKKAVIQVTTNG 127
 OY 271 GDLSSSTGAPDLQMPGGVGI FNGCSKMGAPNDGMSRYGSISSASDCSSLPASALQAG 330
 DB 128 GDLSSN--QFDLAPGSGVGIYNGCTQSGAPADGMSRYGSISSASDCSSLPASALQAG 184
 OY 331 CKRPFNFQADNPSMTYKEVTCPEKITAKTGCGR 365
 DB 185 CKRPFNFQADNPSINFNOYTCPEKITAKTNCGR 219

RESULT 4

O9JH91 PRELIMINARY; PRT; 219 AA.

AC O9JH91; PRELIMINARY; 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxId=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohno K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus";
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB045172; BAA98042.1; -;
 DR HSSP; P43316; 2ENG.
 DR InterPro; IPR000334; GH 45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 SQ SEQUENCE 219 AA; 23126 MW; A712EF3F3CAB041C CRC64;

Query Match 38.5%; Score 777.5; DB 14; Length 219;
 Best Local Similarity 64.7%; Pred. No. 2.6e-46;
 Matches 139; Conservative 30; Mismatches 41; Indels 5; Gaps 3;

OY 152 IVSGASGNGVTRRYMDCKKASGMPGKANVSPYKSCNKDGVTAL--SDSNVQSGCNGN 210
 DB 8 LISWVGDSGRTRRYMDCKKASGMPGKANVSPYKSCNKDGVTAL--SDSNVQSGCNGN 210

[illegible]

RESULT 5

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ID      O9JH87;          PRELIMINARY;          PRT;          219 AA.
AC      O9JH87;
DT      01-OCT-2000 (TrEMBLrel. 15, Created)
DT      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT      01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE      Family 45 cellulase homologue.
OS      unclassified eukaryotes.
OC      Eukaryota.
OX      NCBI_TaxId=42452;
RN      1)
RP      SEQUENCE FROM N.A.
RA      Onizuka K., Onizuka M., Moriya S., Kudo T.;
RT      "Diverse genes of family 45 cellulase homologues of the symbiotic
RT      protists in the hindgut of termite Reticulitermes speratus."
RL      Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
RS      EMBL; AB045176; BAA98046.1; -.
DR      HSSP; PA3316; 2ENG.
DR      InterPro; IPR000334; GH_45.
DR      Pfam; PF02015; Glyco_hydro_45; 1.
DR      PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ      SEQUENCE          219 AA; 23134 MW; 4BDEFEBC9ACC772D CRC64;

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Query Match	38.2%	Score 771.5	DB 14	Length 219
Best Local Similarity	62.5%	Pred. No. 6.7e-46		
Matches 135, Conservative	33	Mismatches 43	Indels 5	Gaps 3

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QY 151 SIVSGGASGNGVYTTTRVMDCCCKASCSMPGRANYS PAKSNCNDC VTLV -SPSNVQSGCNG 209
Db 7 AFISNLSLADSGTTRVMDCCCKSCGMEKANANDKPIIDTCAKDOTTVAASNDIVKSGCDGG 66
QY 210 NSVMCNDNQPMVAIVNDNLAYGFAAAALISGGGSESRMCCCELTETSTSVAGKKNVIVTNT 269
Db 67 DGFMCYDGTTPMqVSVSLSYGFAAAACC -GGESGACCGCGELTFTSGPVMGKKVYQITNT 125
QY 270 GGDIGSSSTGAHFDLQMPGGGVGVI PNGCSTKQWGA PANDGMSRYGIGISASPDSSLPSALQA 329
Db 126 GGDIGLSN---CPDLAI PGGGVGVIYNGCTAOSGAPSDGMSRSRYGVSVSSRSSECLPGLQA 182
QY 330 GCKMRFNNPKADNPSTMYKEYTCPEIKETPAKTCGSR 365
Db 183 GCQMRFDMPQONADNPISINSQVSCBEIILAKTHCNR 218

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RESULT 6

ID	Q9UH83; PRELIMINARY; PRT; 220 AA.
AC	Q9UH83;
DT	01-OCT-2000 (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT	01-MAR-2002 (TrEMBLrel. 15, Last annotation update)
DE	Family 45 cellulase homologue.
OS	Unclassified eukaryotes.
OC	Eukaryota.
OX	NCBI_TaxID=42452;
ON	[1]
RP	SEQUENCE FROM N.A.
RA	Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT	"Diverse genes of Family 45 cellulase homologues of the symbiotic

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RT   proteins in the hindgut of termite Reticulitermes speratus.".
RL   Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR   EMBL: AB045167; BAA98037.1; -.
DR   EMBL: AB045166; BAA98036.1; -.
DR   HSSP: P43316; 2BNC.
DR   InterPro: IPR000334; GH_45.
DR   Pfam: PF02015; Glyco_hydro_45; 1.
DR   PROSITE: PS01140; GLYCOSTL_HIDROL_F45; UNKNOWN_1.
SQ   SEQUENCE   220 AA; 23108 MW;  97738D831BCA5F3 CRC64;

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Query Match	Score	DB	Length
38.1%	769	14	220

Matches	138;	Conservative	29;	Mismatches	45;	Indels	6;	Gaps	4;
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[illegible]

RESULT 7

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ID      Q9JH89;                                PRF;    219 AA.
AC      Q9JH89;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DT      Family 45 cellulase homologue.
DE      unclassified eukaryotes.
OS      Eukaryota.
OC      Eukaryota.
OX      NCBI_TaxId=42452;
RN      [1]
RP      SEQUENCE FROM N.A..
RA      Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT      "Diverse genes of family 45 cellulase homologues of the symbiotic
RT      RT diversifies in the hindgut of termite Reticulitermes speratus";
RL      Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL      EMBL; AB045174; BAA98044.1; -.
DR      HSSP; P43316; ZENG.
DR      InterPro; IPR000334; GH_45.
DR      Pfam; PF02015; GLYCO_HYDRO_45.1.
DR      ProSite; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN.1.
SQ      SEQUENCE 219 AA; 23033 MW; CA295CABDF333199 CQC64;

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Query Match	38.0%;	Score 767.5;	DB 14;	Length 219;
Best Local Similarity	64.7%;	Pred. No. 1.3e-45;		
Matches '134; Conservative	29;	Mismatches 39;	Indels 5;	Gaps 3;

2

[illegible]


```

OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB045175; BAA98045.1; -.
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 219 AA; 23030 MM; 179BFI344C6D024 CRC64;

Query Match 37.6%; Score 759.5; DB 14; Length 219;
Best Local Similarity 64.3%; Pred. No. 4.5e-45;
Matches 133; Conservative 26; Mismatches 43; Indels 5; Gaps 3;

OY 160 NGVTRRYWDCCKASGSMFGKANVSSPVKSCNKGVTAL-SDSNVQSGGNGSNVYCNQDQ 218
DB 16 SKGTRRYWDCCKSGCGMEKKNVDPKPIDTCAKDGTRVANSNTVYSGCDGGTGYCTDQT 75
OY 219 PMAVNDNLAYGFAAAAIISGSGESRWCCSCFELFTSTSVAGKXNVIQVNTNGDLSSTG 278
DB 76 PMQVSDSLSYGFAAAACC-GGESSGACCGCYELFTTSGPVNGKXMI VQITNTGGDLGSN-- 132
OY 279 AHFDLQMPGGVGIFNGCSKQMGAPNDGWSRGYSGISSASDCSSLPALQAGCKRFRNWF 338
DB 133 -QFDLAIFGGGVGIVNGCTSGSGAPADGWSRGYSSRSRSECSQLPSGLQAGCQWRPDMF 191
OY 339 KNAADPSMTYKEVTCPEKITAKTGCSR 365
DB 192 ANADNPINFTNVKCPSELIAKTNCR 218

RESULT 12
OY 09JH86 PRELIMINARY; PRT; 219 AA.
AC 09JH86;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB045177; BAA98047.1; -.
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 219 AA; 23158 MM; ECD686EABEDIDDI CRC64;

Query Match 37.5%; Score 756.5; DB 14; Length 219;
Best Local Similarity 63.3%; Pred. No. 7.2e-45;
Matches 131; Conservative 29; Mismatches 42; Indels 5; Gaps 3;

OY 160 NGVTRRYWDCCKASGSMFGKANVSSPVKSCNKGVTAL-SDSNVQSGGNGSNVYCNQDQ 218
DB 16 SKGTRRYWDCCKSGCGMEKKNVDPKPIDTCAKDGTRVANSNTVYSGCDGGTGYCTDQT 75
OY 219 PMAVNDNLAYGFAAAAIISGSGESRWCCSCFELFTSTSVAGKXNVIQVNTNGDLSSTG 278
DB 76 PMQVSDSLSYGFAAAACC-GGESSGACCGCYELFTTSGPVNGKXMI VQITNTGGDLGSN-- 132

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OY 279 AHFDLQMPGGVGIFNGCSKQMGAPNDGWSRGYSGISSASDCSSLPALQAGCKRFRNWF 338
DB 133 -QFDLAIFGGGVGIVNGCTAGSAPSDGWSRGYSSRSRSECSQLPSGLQAGCQWRPDMF 191
OY 339 KNAADPSMTYKEVTCPEKITAKTGCSR 365
DB 192 QNADNPINFTNVKCPSELIAKTNCR 218

RESULT 13
OY 09JH94 PRELIMINARY; PRT; 221 AA.
AC 09JH94;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB045169; BAA98039.1; -.
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 221 AA; 23220 MM; BA84CEB0A8C46372 CRC64;

Query Match 37.4%; Score 754.5; DB 14; Length 221;
Best Local Similarity 63.3%; Pred. No. 1e-44;
Matches 131; Conservative 30; Mismatches 41; Indels 5; Gaps 3;

OY 160 NGVTRRYWDCCKASGSMFGKANVSSPVKSCNKGVTAL-SDSNVQSGGNGSNVYCNQDQ 218
DB 17 SKGTRRYWDCCKSGCGMEKKNVDPKPIDTCAKDGTRVANSNTVYSGCDGGTGYCTDQT 76
OY 219 PMAVNDNLAYGFAAAAIISGSGESRWCCSCFELFTSTSVAGKXNVIQVNTNGDLSSTG 278
DB 77 PMAVNDLSLGFAAAAS-GGEKXACCGCYELFTTSGPVNGKXIVQITNTGGDLGSN-- 133
OY 279 AHFDLQMPGGVGIFNGCSKQMGAPNDGWSRGYSGISSASDCSSLPALQAGCKRFRNWF 338
DB 134 -QFDLAIFGGGVGIVNGCTAGSAPADGWSRGYSSRSRSECSQLPSGLQAGCQWRPDMF 192
OY 339 KNAADPSMTYKEVTCPEKITAKTGCSR 365
DB 193 QNADNPINFTNVKCPSELIAKTNCR 219

RESULT 14
OY 09JH85 PRELIMINARY; PRT; 218 AA.
AC 09JH85;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB045178; BAA98048.1; -.
DR HSSP; P43316; 3ENG.

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[illegible]